Abstract: Comparison of Analyzing and Quantifying Total PCBs by Different Methods at the New Bedford Harbor Superfund Site OU#3 Site

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The New Bedford Harbor Superfund site, located in Buzzards Bay in southeastern Massachusetts, is one of the most highly PCB contaminated marine estuaries in the world. The overall New Bedford Harbor Superfund Site encompasses nearly 18,000 acres area total, extending from the Upper Harbor (187 acres), Lower Harbor (750 acres) New Bedford Harbor, and adjacent areas of Buzzards Bay (17,000 acres). To date, approximately 205,000 cubic yards of contaminated sediment have been removed from New Bedford Harbor. The outer harbor area termed Operable Unit #3 (OU#3), is the area where recent Remedial Investigation/ Feasibility Study (RI/FS) samples were collected and analyzed for PCB analysis.

Several different methods of analyzing and quantifying total PCB's have been utilized over the years, and the new phase of investigations at OU#3 offered an opportunity to perform and evaluate a few different methods of analyzing and quantifying total PCBs. Since the primary data users of the RI/FS had several different data needs and requirements, analytical and quantitation methods that satisfied the varying criteria were chosen. EPA Method 8270C-GC/MS-SIM, modified for the analysis of the 209 PCB congeners was performed as the primary analytical method. This method alone supported several end user needs. The data user's needs included; the historical long-term monitoring of the 18 NOAA congeners by the US EPA, monitoring of edible seafood using 136 congeners by the Massachusetts Division of Marine Fisheries, and human and ecological risk assessments encompassing the EPA/WHO dioxin-like PCB congeners and total PCB quantitation by summation of the 209 PCB congeners.

Alpha Analytical of Mansfield, MA, performed the 8270C-GC/MS-SIM for the 209 PCB congeners and also offered to perform PCB analysis by Method 8082-GC/ECD for Aroclors, as well as Method 8270C-GC/MS-SIM for PCB Homologues. A sub set of sediment and tissue samples from the NBH OU#3 RI/FS data set were tested by these different analysis and quantitation methods for reporting total PCB's. The same extracts

were used to perform all analyses to minimize variables due to heterogeneity of the matrices. The comparison of these total PCB results and the analytical methodologies will be discussed in detail. The pros and cons of these comparison findings will be evaluated based on the analytical methodologies, the project specific Measurement Performance Criteria and Data Quality Objectives.

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